```
taatcagtttattttctttcadataaaaaataactatgagcgagctaacat 471
                                             ttcatgcttcctgtgatttcatccaactacttaccttgcctacgatatcccctttatctc
                                                                                                                                                                                                                                                                                     aaccactgctgctgcaaccactgcgaccactgctgctcctaccactgcaaccaccgctgc
                                                                                           ttcatgcttcctgtgatttcatccaactacttaccttgcctacgatatcccctttatctc
                                                                                                                                                                        tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
                                                                                                                                                                                                                      ttctaccactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaa
                                                                                                                                                                                                                                       ttctaccactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaa
                                                                                                                                                                                                                                                                                                     aaccactgctgctgcaacaactgcgaccactgctgctcctaccactgcaaccaccgctgc
                                                                                                                                                                                                                                                                                                                                                                  tgctccagctgacacgtatccagctactggtcctgctgatgatgaagcccctgatgctga
                                                                                                                                                         tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaattgggtcacaacta
                                                                                                                                                                                                                                                                                                                                                     tgctccagctgacacgtatccagctactggtcctgctgatgatgaagcccctgatgctga
                                                                                                                             420
                                                                                                                                                                                         360
                                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                         360
                                                                                                                                                                                                                         300
                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                      180
                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'us-09-525-361a-23.rng
                     δ
                                                         В
                                                                                      δÃ
                                                                                                                                                  Qy
                                                                                                                      g
                                                                                                                                                                                      Вþ
                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                    88668
888
                                                                                                                                                                                                                                                                  Query
Best L
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                        manufacture of a medicament for treating breast cancer in a patient. Antigen presenting cells incubated in the presence of at least one polypeptide are also useful for treating breast cancer.
                                                                                                                                                                                                                                                                                                                                  Sequence 480
                         181
                                                         123
                                                                                       121
                                                                                                                                                                                                                                                          / Match
Local Similarity
                                                                                                                       63
                                                                                                                                                      61
                                                                                                                                                                        3 ctttgaagcatttttgtctgtgctccctgatcttcaggtcaccaccatcagagtctttagc
                                                                                                                                                                                             1 ctttgaagcatttttgtctgtgctccctgatcttcaggtcaccaccaccatgaagttcttagc
aaceactgctgctgcahCabctgcgaccactgctgctcctaccactgcaaccaccgctgc
                                                                                                            agtcctggtactcttgggagtttccatctttctggtctctgcccagaatccgacaacagc
                                                                                                                             agtcctggtactcttgggagtttccatctttctggtctctgccagaatccgacaacagc
                                                              tgctccagctgacacgtatccagctactggtcctgctgatgatgaagcccctgatgctga
                              tgctccagctgacacgtatccagctactggtcctgctgatgatgaagcccctgatgctga
                                                                                                                                                                                                                                                   463;
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                             BP; 121 A; 132 C;
                                                                                                                                                                                                                                                               95.2%;
                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                            Score 448.4;
                                                                                                                                                                                                                                                                                                                           87 G; 140 T; 0 other;
                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                               No.
                                                                                                                                                                                                                                                               2e-113;
                                                                                                                                                                                                                                                                            DB 20;
```

6;

Indels Length 480;

1;

Gaps

1

62

60

```
RESULT
AAC79431
                                                                                                                                                                                                      밁
                                                                                                                                                                                                                  Q
                                    09-APR-1999;
02-JUL-1999;
                                                                                                          Human; breast breast cancer;
                                                                                                                            cDNA sequence of human breast tumour clone 1016F8
                                                       10-APR-2000; •2000WO-US09688
                                                                                              Homo sapiens
                                                                                                                                         07-FEB-2001 (first entry)
                                                                                                                                                        AAC79431;
                                                                                                                                                                     AAC79431 standard;
                                                                                                                                                                                                      422
                                                                                                                                                                                                                  421
                                                                                                                                                                                  4
                                                                                                                                                                                                 taatcagtttattttctttcaaataaaaataactatgagcaacaaaaaa
                                                                                                                                                                                                          tumour antigen;
                                    99US-0288950
99US-0346327
                                                                                                           vaccine;
                                                                                                                                                                     CDNA;
                                                                                                                                                                    ВP
                                                                                                               cytostatic;
                                                                                                              immunotherapy;
                                                                                                                                                                                                               470
```

(CORI-)

CORIXA

CORP

χ̈́L

This sequence encodes a human breast tumour protein immunogenic fragment of the invention. The polypeptides or nucleic acids encoding them are useful in vaccines and pharmaceutical compositions for manufacture of medicaments for inhibiting the development of breast cancer in a patient. They can also be used to treat breast cancer. Antibodies against these polypeptides can be used to detect and monitor progression of breast cancer in patients. Primers and probes derived from the polynucleotides encoding the breast proteins are useful for detection of breast cancer. Peripheral blood cells from a patient incubated in the presence of at least one polypeptide, such that T cells proliferate, are useful in

WPI; 2000-638568/61

SG,

Xu J, Dillon

200

(CORI-) CORIXA CORP

Claim

Page 58;

70pp; English.

New breast tumour protein genes used, or for diagnosis of breast cancer

in vaccines

for immunotherapy,

WPI; Reed SG,

1999-405486/34

17-JUL-1998; 24-DEC-1997; 24-DEC-1997; 17-JUL-1998;

98US-0118627. 97US-0998253. 97US-0998255. 98US-0118554.

08-JUL-1999

W09933869-A2

22-DEC-1998;

98WO-US27416

Homo

sapiens

breast Breast

cancer

protein; immu
development;

therapy;

SS

밁 20 В Ş

362 361 303 301 243

ttcatgottcctgtgatttcatccaacttacttgcctacgatatcccctttatctc

420

361 360 302 300

421

ttcatgcttcctgtgatttcatccaactacttaccttgcctacgatatcccctttatctc

tggtagagtgtgtccctgabatggaatcagcttgagtcttctgcaattgggtcacaacta

ttctaccactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaa ttctaccactgctcgtaaagacattccagttttacccaaatgggttggggatctcccgaa aaccactgctgcahccactgcgaccactgctgctcctaccactgcaaccaccgctgc

tggtagagtgtgtccctgagatggaatcagcttgagtcttctgcaatt-ggtcacaacta

immunogenic fragment; vaccine; detection;

immunogenic fragment.

DNA encoding human breast tumour protein

08-SEP-1999

(first entry)

AAX84202;

RESULT AAX84202

ω

AAX84202 standard; cDNA;

480

δÃ 뭐

B

183 241

240

242

180

122 120

182

В δõ Ъ Q В Q 망 õ В ρ Вþ õ

421 421 361 361 301 301 241 241 181 181 121 121

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Run on:
                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                                                                     Match
              N_Geneseq_032802:*
1: /SIDS1/gcgdata/
2: /SIDS1/gcgdata/
                                                                                                                                                                                                                                                                                                                               | SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1991_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1992_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1993_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1994_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1995_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1995_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA1998_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA2000_DAT:*
| SIDSI/gcgdata/geneseq/geneseqn-embl/NA2001ADAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1736436 seqs, 858457221 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ctttgaagcatttttgtctg.....aactatgagcgagctaacat 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-525-361A-23
471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 4.5
Copyright (c) 1993 - 2000 Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS1
                                                                                                                                                                                     Length
           471
471
480
489
489
497
578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5, 2002, 04:39:04 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
                                                                                                                                                                                     В
                                                                                                                                                                                     IJ
                                                                                            AAA54120
AAF85500
AAX84202
AAC79431
                         AAX00704
AAX00644
AAZ40783
AAC79470
           AAI67224
                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time 211.95 Seconds ...
(without alignments)
3815.365 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3472872
Breast cancer prot
Nucleotide sequenc
DNA encoding human
cDNA sequence of h
Human secreted pro
Human secreted pro
Secreted protein E
cDNA sequence of h
B511s cDNA sequenc
                                                                                                                                                           Description .
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT

AAA54120

AAA5

XX

AC

AAA5

XX

AC

AAA5

XX

AC

DT

08-F

XX

DE

Brea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Breast cancer protein BCH1 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA54120 standard; DNA; 471 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA54120;
```

#.0 LJ./	A 6 13 7 1	6 13 7 1	4.6 13.7	4.6* 13.7	4.8 13.8 3	4.8 13.8 1	65 13.8	5.4 13.9	14.9	94 20.0	81.4 38.5	81.4 38.5	81.4 38.5	86.4 39.6	02.8 43.1	02.8 43.1	47.2 52.5	55.6 54.3	55.6 54.3	71.4 57.6	86.8 60.9	98.8 63.4	00.8 63.9	00.8 63.9	.8 63.9	42	43 94.1	43 94.1	43 94.1	46.2 94.7	46.2 94.7	46.4 94.8	46.8 94.9	.8 94.9	447 94.9	47 94.9
12 21	; ~	j č		ا د	6	26	34 1	17 2	97 2	0 2	97 2	97 2	97	21 2	29 2	29 ]	91	66	64	73	92	01	80	80	80	188 22	71	71 :	71	73	72	44	53	53	82	82
AAA59241	AAA5924	MAY I / ZZ	7777777	2000	AA07516	AAS8310	AAQ8483	AAZ4430	868XAV	AAS8772	AAD1867	AAX5558	AAV3199	AAD1866	AAX5557	AAV3198	AAF9339	AAF933	AAF933	AAA541:	AAD186	AAS877	AAD186	AAX555	AAV319		AAC974	AAF442	AAZ650	AAD186	AAD186	AAZ917	AAX555	AAV319	AAX555	AAV319
D, C, B	E, C	gene CAG	Glutamine rich reg	, ,,	encouring nove	oncoding and		iman SCA7 genomi	ocerebellar a	encoding nove	BS106 gene-	BS106 Clone 120981	מסבסט שבוים	BS106 gana-	BS106 close 166388	to billing log	DNA encoding	DNA encoding	encoding pro	st Cancer	n Belok gang-	encoding some	n RS106 gang-		BS106 polymic looks	and rode	PROTIEG (	ane-bound	and the get	n being gene-	n Being gang-	מ מ	106	210	5106	106 polynuciao

## ALIGNMENTS

PR 1: PR 1:	PR 1:		PD 2	XX W		) F	FT		OS H						×
12-NOV-1999; 15-NOV-1999;	15-MAR-1999; 12-NOV-1999;	5-MAR-2000; 2	21-SEP-2000.	WO200055629-A2.	•		CDS	ey	Homo sapiens.		CN5: BCO2: BC	vmph node: me	ntibody; oesi	reast cancer	
99US-0440370. 99US-0440493.	99US-0268865. 99US-0439878	15-MAR-2000; 2000WO-US06952.			/product= BCH1 protein	/*tag= a	47319	Location/Qualifiers		bchz; bchz; bchz; bchz; bcJ/; bCf3; human; ds.	BCN5: BCO2: BCX2: BCX3: BCN3: BCN3; BCN1; BCN1; BCN2;	otastases tumour nona noco no tumuna response;	antibody; oestrogen receptor: anti-postrogen: immunication;	Breast cancer; diagnosis; prognosis; detection: coroning.	France: Four couring sequence.